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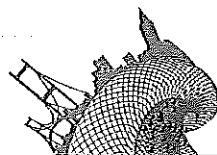
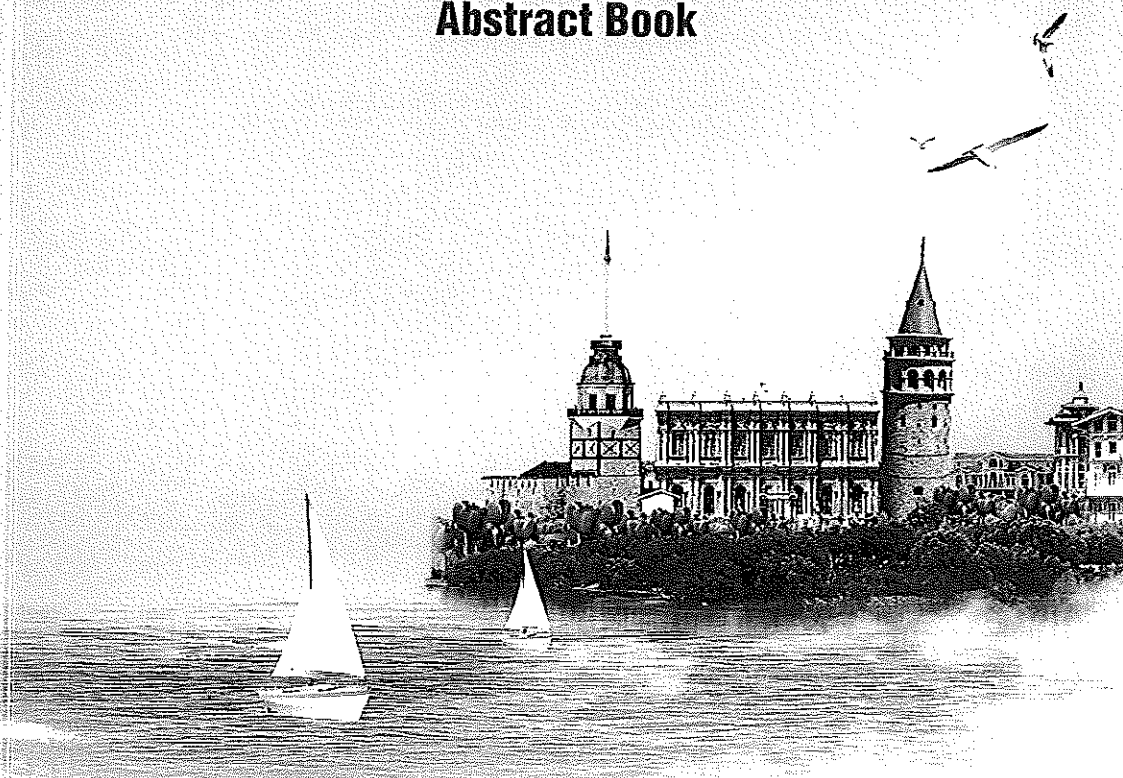


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Comparative genome sequences analysis of *Bacillus sonorensis* 112 isolated from a primary starter used for production of Sudanese traditional bread, Gergoush, and *B. licheniformis* DSM13T

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Bacillus sonorensis was first isolated from the Sonoran Desert soil. Taxonomic studies have indicated is closely related to *B. licheniformis*. The two species can be phenotypically distinguished based on colonies pigmentation, but in general little is known about the genomic, evolutionary and phylogenetic status of *B. sonorensis* species. The closely related species *B. licheniformis* is exploited industrially for large-scale production of many enzymes such as proteases, amylases and lipopeptide surfactants. These enzymes are used; to produce detergents, for liquefaction of starch, for oil recovery and in the paper and textile industries. *B. sonorensis*, *B. licheniformis* and *B. subtilis* species strains were isolated in high numbers from a primary starter used for the production of African traditional bread; Gergoush in Sudan. An earlier study on the antimicrobial susceptibility profiles of these species strains to frequently used antibiotics indicated that *B. sonorensis* and *B. subtilis* species were susceptible to clindamycin whereas *B. licheniformis* species strains were intrinsically resistant. To further enhance our limited knowledge and to explore the technological relevance of *B. sonorensis* species, strain L12 from our previous study was completely genome sequenced using the Illumina HiSeq platform. The sequences were assembled into contigs using CLC genomic workbench (CLC Aarhus, Denmark) which was also used to determine the nucleotides sequences statistics. Transfer RNA genes and rRNA operons were predicted using tRNAscan-SE and RNAmmer programs respectively. Open reading frames (ORFs) were predicted using IOGMA® software version 3.8 (Genostar Bioinformatics Software & Services©). Auto-annotation of the predicted ORFs was based on BLASTP analysis against GenBank database. Evolutionary dynamics of strain L12 and *B. licheniformis* DSM13T were further observed using the Mauve software for Multiple Genome Alignment. The latest data on the complete genome sequence of *B. sonorensis* strain L12 and comparative analysis with *B. licheniformis* DSM13T will therefore be presented. To our knowledge, this is the first genome sequence of a *B. sonorensis* strain. The information obtained from the genome of this species will provide valuable insight for both evolutionary and phylogenetic aspects of these two closely related species.

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The effect of heat on genetically modified

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Genetically modified organisms of food safety area. Although they since they were first commercialized rapidly. Because of this strong reaction on labelling of GMOs and GM foods, enforce the labelling of food developing reliable methods for food science area since early 20th century which is based on detection of novel DNA are used for this purpose. ELISA methods are not suitable because of the degradation effect on yield, there are limits of PCR method. The aim of the present study is to detect GM soya in cookies. Cookies of GM soya were prepared and subjected to heat on DNA quality of these samples. A novel sequence which is present in both GM and non GM soya was detected. PCR is significant for the presence of practically low levels of